

IN THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims:

1-39 (Cancelled)

40. (New) A device for the isolation and/or purification of nucleic acid molecules comprising at least two layers, a first layer being adapted to bind and/or inactivate inhibitors of the activity of reagents or enzymes used in nucleic acid manipulation and a second layer being adapted to separate a plurality of nucleic acid molecules with respect to their size and wherein said first layer is a first phase of a gel and said second layer is a second phase of said gel.
41. (New) The device of claim 40, wherein said first layer is arranged above the second layer.
42. (New) The device of claim 40, wherein said gel is an agarose gel or a polyacrylamide gel.
43. (New) The device of claim 40, wherein said first layer comprises polyvinylpyrrolidone (PVP), polyvinylpolypyrrolidone (PVPP), CTAB, EDTA, EGTA, cyclodextrins, proteins, (poly)peptides, antibodies, aptamers, lectins, nucleic acids or ion-exchanger.
44. (New) The device of claim 40, wherein said second layer is substantially free of PVP, PVPP, CTAB, EDTA, EGTA, cyclodextrins, proteins, (poly)peptides, aptamers, antibodies, lectins, nucleic acids or ion-exchanger.
45. (New) The device of claim 40, wherein the device is electrically biased to enhance flow of at least one sample through the layers.
46. (New) The device of claim 40, wherein said first layer comprises sample loading means.
47. (New) The device of claim 46, wherein said loading means are provided in an array in an upper portion of the first layer, defining an array of columns, each column being capable of isolating nucleic acid molecules.
48. (New) The device of claim 40, wherein said first layer is arranged below the second layer.

49. (New) The device of claim 48, which is a column comprising said first and said second layer.
50. (New) The device of claim 48, wherein said second layer is a first phase of a column and said first layer is a second phase of said column.
51. (New) The device of claim 48, wherein said first layer is a matrix comprising PVP, PVPP, CTAB, EDTA, EGTA, cyclodextrins, proteins, (poly)peptides, aptamers, antibodies, lectins, nucleic acids or ion-exchanger.
52. (New) The device of claim 48, wherein said second layer is a matrix which is substantially free of PVPP PVP, PVPP, CTAB, EDTA, EGTA, cyclodextrins, proteins, (poly)peptides, aptamers, antibodies, lectins, nucleic acids or ion-exchanger.
53. (New) The device of claim 51, wherein said matrix of said first and/or second layer is selected from the group consisting of agarose, sepharoseTM, sephadexTM, sephacrylTM, BioGelTM, superoseTM and acrylamide.
54. (New) The device of claim 40, wherein said nucleic acid molecule is DNA or RNA.
55. (New) The device of claim 54, wherein said DNA is genomic DNA.
56. (New) The device of claim 54, wherein said nucleic acid molecule is derived from (micro)organisms of soil, sediments, water or symbiotic/parasitic consortia.
57. (New) The device of claim 56, wherein said (micro)organisms are (micro)organisms of aquatic plankton, microbial mats, clusters, sludge flocs, or biofilms.
58. (New) The device of claim 56, wherein said (micro)organism are isolated as consortia of coexisting species.
59. (New) The device of claim 54, wherein said nucleic acid molecules represent a fraction of the metagenome of a given habitat.
60. (New) A method for the isolation of a nucleic acid molecule comprising applying a sample to the device as defined in claim 40.

61. (New) The method of claim 60, wherein a fraction of the metagenome is isolated from a given habitat.
62. (New) A method for the generation of at least one gene library, comprising the steps of
- (a) isolating and/or purifying nucleic acid molecules from a sample using a device as defined in claim 1, and optionally amplifying said nucleic acid molecules;
 - (b) cloning the isolated and/or purified and optionally amplified nucleic acid molecules into appropriate vectors; and
 - (c) transforming suitable hosts with said suitable vectors.
63. (New) The method of claim 62, wherein said suitable hosts are selected from the group consisting of *E. coli*, *Pseudomonas* sp., *Bacillus* sp, *Streptomyces* sp., other actinomycetes, myxobacteria, yeasts and filamentous fungi.
64. (New) A gene library generated from metagenomic nucleic acid molecules from non-planctonic (micro)organisms comprising average insert sizes of at least 50 kB, of at least 55 kB, of at least 60 kB, of at least 80 kB, of at least 90 kB or of at least 100 kB.
65. (New) A gene library generated from metagenomic nucleic acid molecules from planctonic (micro)organisms comprising average insert sizes of at least 85 kB, at least 90 kB, at least 95 kB, at least 100 kB, at least 120 kB, at least 140 kB, at least 160 kB or at least 200 kB.
66. (New) A nucleic acid molecule comprising a DNA as depicted in SEQ ID NO: 1 or a DNA as deposited under EMBL accession number A3496176.
67. (New) A nucleic acid molecule representing a part of the genome of a non-thermophilic crenarchaeota, whereby said nucleic acid molecule has at least one of the following features:
- (a) it contains at least one ORF which encodes a polypeptide having the amino acid sequence SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19,

SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35;

- (b) it comprises the DNA sequence of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34;
- (c) it comprises a portion of at least 20 nucleotides, preferably 100 nucleotides, more preferably at least 500 nucleotides, which hybridize under stringent conditions to the complementary strand of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34;
- (d) it is degenerate as a result of the genetic code with respect to the nucleic acid molecule of (c); or
- (e) it is at least 50% identical with the nucleic acid molecule of SEQ ID NO: 2, SEQ ID NO: 20 or SEQ ID NO: 30, 45% identical with the nucleic acid molecule of SEQ ID NO: 8 or SEQ ID NO: 26, 35% identical with the nucleic acid molecule of SEQ ID NO: 16, SEQ ID NO: 22 or SEQ ID NO: 24 or 30% identical with the nucleic acid molecule of SEQ ID NO: 4, SEQ ID NO: 14, SEQ ID NO: 18 or SEQ ID NO: 28.

68. (New) The nucleic acid molecule of claim 67, which is DNA or RNA.

69. (New) A vector comprising the nucleotide acid molecule of claim 68.

70. (New) A host transfected or transformed with the vector of claim 69.

71. (New) A method for producing a (poly)peptide as encoded by a nucleic acid molecule of claim 67, comprising culturing the host of claim 70 under suitable conditions and isolating said polypeptide from the culture.

72. (New) A (poly)peptide encoded by a nucleic acid molecule of claim 67 or as obtained by the method of claim 71.
73. (New) The (poly)peptide of claim 72 which is glycosylated, phosphorylated, amidated and/or myristylated.
74. (New) An antibody or an aptamer specifically recognizing the (poly)peptide of claim 72 or a fragment or epitope thereof.
75. (New) The antibody of claim 74, which is a monoclonal antibody.
76. (New) A transgenic non-human mammal whose somatic and germ cells comprise at least one gene encoding a functional polypeptide selected from the group consisting of:
- (a) the polypeptide of claim 72;
 - (b) a polypeptide having an amino acid sequence that is at least 60%, preferably at least 80%, especially at least 90%, advantageously at least 99% identical to the amino acid sequence of (a); and
 - (c) a polypeptide having the amino acid sequence of (a) with at least one conservative amino acid substitution.